

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT (other than U.S.): AMRAD CORPORATION LIMITED  
(U.S. only): **Douglas James HILTON**

(ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: AU PROVISIONAL  
(B) FILING DATE: 05-SEP-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HUGHES DR, E JOHN L  
(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: +61 3 9254 2777  
(B) TELEFAX: +61 3 9254 2770

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## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1705 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 45..1340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC AGC	56
Met Ser Ser Ser	
1	
TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG	104
Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val	
5 10 15 20	
TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG	152
Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln	
25 30 35	
TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT	200
Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser	
40 45 50	
GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC	248
Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu	
55 60 65	

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CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val	296
70 75 80	
GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val	344
85 90 95 100	
TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro	392
105 110 115	
GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp	440
120 125 130	
AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr	488
135 140 145	
AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser	536
150 155 160	
ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys	584
165 170 175 180	
GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr	632
185 190 195	
GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu	680
200 205 210	
CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser	728
215 220 225	
GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala	776
230 235 240	
TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC AAG TTC CGG TTG CAA TAC Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr	824
245 250 255 260	
CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG GTG GAG CCC ATT GGC TTG Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu	872
265 270 275	
GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG CTG CCA CAC GCG GTA CGA Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg	920
280 285 290	

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GTC AG<sup>1</sup> GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG AGC GCC TGG AGC 968  
 Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser  
 295 300 305

CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT GAG ATA 1016  
 Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile  
 310 315 320

CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG CTA GAG GCA GTA GTA GCT 1064  
 Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala  
 325 330 335 340

CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA 1112  
 Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro  
 345 350 355

AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG CAA GTA GCT GTG TTA GCG 1160  
 Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala  
 360 365 370

TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG GCT GTT GGA GCT CTG GCA 1208  
 Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala  
 375 380 385

CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT GGG AAG GAT GGA CCG CAA 1256  
 Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln  
 390 395 400

AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG GTG GAA AAG CTT CCA GGA 1304  
 Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly  
 405 410 415 420

ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC TTC AGC TGATTTTCATC 1350  
 Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser  
 425 430

TGTAACCCGG TCAGACTGGG GGCAGAAAGA GCGGGGGCAG TGGATCCCTG TGGATGGAGG 1410

TCTCAGCTGA AAGTCTGAGC TCTTTTCTTT GACACCTATA CTCCAAACTT GCTGCCGGCT 1470

GAAGGCTGTC TGGACTTCCG ATGTCCTGAG GTGGAAGTCC ACCTGAGGAA TGTGTACAGA 1530

AGTCTGTGTT CCTGTGATCG TGTGTGTATG TGAGACAGGG AGCAAAAGTT CTCTGCATGT 1590

GTGTACAGAT GATTGGAGAG TGTGTGCGGT CTTGGGCTTG GCCCTTCTGG GAAGTGTGAA 1650

GAGTTGAAAT AAAAGAGACG GAAGTTTTTG GAAAAAAAAA AAAAAAAAAA AAAAA 1705

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala
 1           5           10           15
Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
          20           25           30
Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys
          35           40           45
Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp
          50           55           60
Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val
          65           70           75           80
Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr
          85           90           95
Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro
          100          105          110
Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe
          115          120          125
Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr
          130          135          140
Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg
          145          150          155          160
Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu
          165          170          175
Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg
          180          185          190
Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu
          195          200          205
Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
          210          215          220

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Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp  
 225 230 235 240  
 Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe  
 245 250 255  
 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu  
 260 265 270  
 Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro  
 275 280 285  
 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp  
 290 295 300  
 Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu  
 305 310 315 320  
 Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu  
 325 330 335  
 Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu  
 340 345 350  
 Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val  
 355 360 365  
 Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val  
 370 375 380  
 Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys  
 385 390 395 400  
 Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu  
 405 410 415  
 Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser  
 420 425 430

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## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1800 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 128..1396

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTCTCC TAGGAAGCCT CAGTTTGGGA 60  
 GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTGGAC TCTACCTCTC 120  
 CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC 169  
 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala  
 1 5 10  
 GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG 217  
 Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp  
 15 20 25 30  
 GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG 265  
 Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu  
 35 40 45  
 TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT 313  
 Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp  
 50 55 60  
 GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA 361  
 Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu  
 65 70 75  
 CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC 409  
 Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys  
 80 85 90  
 CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC 457  
 Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly  
 95 100 105 110

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TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu 115 120 125	505
AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr 130 135 140	553
CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT GAT AGC Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser 145 150 155	601
CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro 160 165 170	649
CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln 175 180 185 190	697
TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr 195 200 205	745
CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro 210 215 220	793
CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg 225 230 235	841
GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu 240 245 250	889
CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG TCC Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser 255 260 265 270	937
ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala 275 280 285	985
GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala 290 295 300	1033
GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr 305 310 315	1081
GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln 320 325 330	1129

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CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC      1177
Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser
335                               340                               345                               350

CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG      1225
Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln
355                               360                               365

GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG CGA CTG GTG      1273
Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val
370                               375                               380

GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT GGG      1321
Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly
385                               390                               395

AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG      1369
Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val
400                               405                               410

GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT      1416
Asp Arg Arg Pro Gly Ala Pro Asn Leu
415                               420

CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA      1476

GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGA GCCCATTTCT GTGAGACCCT      1536

GTATTTCAAA TTTGCAGCTG AAAGGTGCTT GTACCTCTGA TTTCACCCCA GAGTTGGAGT      1596

TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG      1656

AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG      1716

TCCTTGGCTC TTGGCCTTTC CCCTGTCAGG GGTTGTGCAG GTGTGAATAA AGAGAATAAG      1776

GAAGTTCTTG GAGATTATAC TCAG      1800

```

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala
 1             5             10             15

Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
20             25             30

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Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys  
 35 40 45  
 Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu  
 50 55 60  
 Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val  
 65 70 75 80  
 Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr  
 85 90 95  
 Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro  
 100 105 110  
 Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe  
 115 120 125  
 Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr  
 130 135 140  
 Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg  
 145 150 155 160  
 Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly  
 165 170 175  
 Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg  
 180 185 190  
 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr Arg Leu  
 195 200 205  
 Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly  
 210 215 220  
 Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg Ala Ser  
 225 230 235 240  
 Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys  
 245 250 255  
 Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val  
 260 265 270  
 Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu  
 275 280 285  
 Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr  
 290 295 300  
 Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr  
 305 310 315 320  
 Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu  
 325 330 335

SUBSTITUTE SHEET (Rule 26)

Val	Glu	Pro	Gln	Val	Asp	Ser	Pro	Ala	Pro	Pro	Arg	Pro	Ser	Leu	Gln	
340								345	350							
Pro	His	Pro	Arg	Leu	Leu	Asp	His	Arg	Asp	Ser	Val	Glu	Gln	Val	Ala	
355						360		365								
Val	Leu	Ala	Ser	Leu	Gly	Ile	Leu	Ser	Phe	Leu	Gly	Leu	Val	Ala	Gly	
370					375			380								
Ala	Leu	Ala	Leu	Gly	Leu	Trp	Leu	Arg	Leu	Arg	Arg	Gly	Gly	Lys	Asp	
385					390			395							400	
Gly	Ser	Pro	Lys	Pro	Gly	Phe	Leu	Ala	Ser	Val	Ile	Pro	Val	Asp	Arg	
					405			410				415				
Arg	Pro	Gly	Ala	Pro	Asn	Leu										
420																

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

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## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(A/G)CTCCA(N)GC(C/T)CTCCA

15

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

(A/G)CTCCA(N)GG (A/G)CTCCA

15

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

(A/G)CTCCA(C/T)T T(A/G)CTCCA

15

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## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGTCCACGG TGGAGCCCAT TGGCT

25

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCACACGCGG TACGAGTCAG TGCCAGGGAC

30

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCAAGTTCA GCCTGGTTAA G

21

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## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

24

CTTATGAGTA TTTCTTCCAG GGTA

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

24

CCCTTCATTG ACCTCAACTA CATG

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

24

CATGCCAGTG AGCTTCCCGT TCAG

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## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTCCTCCA GGGGTCCAGT ATGG

24

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGGCCTCC AGAGGGT

17

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCCTGTACT TGGAGTCCAG G

21

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## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30

GGAAAGCTGT GGC GTGATGG CCGTGGGGCA

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

22

GGGCGGAGGC CGCTGGCGGG CG

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

23

TTATCAGCTG AAGTTCTCTG GGG

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## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

G/ACTCCANGCG/A CTCAA

15

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCTTCTAGA TCCCCCTGCC CCCAAGCT

28

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACTTTCTAGA TTATTGCTCC AAGGGGTCCC TGTG

34